



# Blast 2 Sequences results

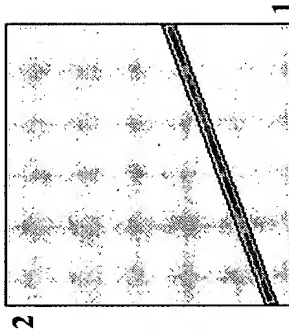
PubMed Entrez BLAST OMIM Taxonomy Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lc|seq\_1 Length 2112 (1 .. 2112)

Sequence 2 lc|seq\_2 Length 5859 (1 .. 5859)



Sequence 1  
Sequence 2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 4061 bits (2112), Expect = 0.0  
Identities = 2112/2112 (100%)  
Strand = Plus / Plus

PEICAD-Byronia, N. J.

EXHIBIT  
E

Query: 1 ggcaatgggtcgaaaattcatagaaattttgtgtgaggtgcgtagcggctctgtacaggggtg 60  
|||||  
Sbjct: 402 ggcaatgggtcgaaaattcatagaaattttgtgtgaggtgcgtagcggctctgtacaggggtg 461  
  
Query: 61 ctgctggagagatctctgtgtctcaggtagggcgacaaatggagaggtgttagttgccccctg 120

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|||||
Sbjct: 462 ctgcgcggagatctctggtctcaggtagggcgacaatggagagggttagttgccccctg 521

Query: 121 tatcgctctctgcgtggcgcattgggtcatcctgccccggacatatgatattccgctagag 180
|||||
Sbjct: 522 tatcgctctctgcgtggcgcattgggtcatcctgccccggacatatgatattccgctagag 581

Query: 181 gattactgatatagtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 240
|||||
Sbjct: 582 gattactgatatagtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 641

Query: 241 gggcctgtccctcttgtcccgccctgtcctcactttttcacaaatcaaaaaaatgggcgaagc 300
|||||
Sbjct: 642 gggcctgtccctcttgtcccgccctgtcctcactttttcacaaatcaaaaaaatgggcgaagc 701

Query: 301 ccttcttgttctatagttcttctatagtttcatacgaaaaattacacataattatcaatagctt 360
|||||
Sbjct: 702 ccttcttgttctatagttcttctatagtttcatacgaaaaattacacataattatcaatagctt 761

Query: 361 attcgcttaaaaggaggagtaattgggcgcgcaaaaggaggagtaattgggcgcgcaaaaggaggt 420
|||||
Sbjct: 762 attcgcttaaaaggaggagtaattgggcgcgcaaaaggaggagtaattgggcgcgcaaaaggaggt 821

Query: 421 aattgggcgcgcaaaaggaggagtaattgggcgcgcatatcggttgtttacatggggaggaatcc 480
|||||
Sbjct: 822 aattgggcgcgcaaaaggaggagtaattgggcgcgcatatcggttgtttacatggggaggaatcc 881

Query: 481 ccttaatcatttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 540
|||||
Sbjct: 882 ccttaatcatttctcccatgggaaagacacacaaagtggccgcagaccgggccttcgac 941

Query: 541 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatgcgcaatccgccc 600
|||||
Sbjct: 942 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatgcgcaatccgccc 1001
```

Query: 601 cgcctgcaggcgctcaagctcatgcatttaatatagaccactgcgggcgcgcgatggct 660  
|||||  
Sbjct: 1002 cgcctgcaggcgctcaagctcatgcatttaatatagaccactgcgggcgcgcgatggct 1061  
|||||

Query: 661 gatgatgtgcgccatgaaatcggtggtgcccgcacattcgcgcaatcgacggcatgaaaaac 720  
|||||  
Sbjct: 1062 gatgatgtgcgccatgaaatcggtggtgcccgcacattcgcgcaatcgacggcatgaaaaac 1121  
|||||

Query: 721 catgacctgagagcctgacccccgctgttcgaggagctagccgcgtgcggtgttgacctat 780  
|||||  
Sbjct: 1122 catgacctgagagcctgacccccgctgttcgaggagctagccgcgtgcggtgttgacctat 1181  
|||||

Query: 781 gatgacctgcaaaagatgatcgtgacagtcggcggttggtcgatgaggcgcaatagac 840  
|||||  
Sbjct: 1182 gatgacctgcaaaagatgatcgtgacagtcggcggttggtcgatgaggcgcaatagac 1241  
|||||

Query: 841 taccgccaggaggcaagcgcggaactcctctagtgacgtggaccttcgcggagttacattccgt 900  
|||||  
Sbjct: 1242 taccgccaggaggcaagcgcggaactcctctagtgacgtggaccttcgcggagttacattccgt 1301  
|||||

Query: 901 cgtatgcggcggtcgaaccactgggccattctcgaccgtcaaacgggtattccatctc 960  
|||||  
Sbjct: 1302 cgtatgcggcggtcgaaccactgggccattctcgaccgtcaaacgggtattccatctc 1361  
|||||

Query: 961 ggtagtaagtattccgtgctgctgttccagcacgtctctagttctcgccaatcttgatcgg 1020  
|||||  
Sbjct: 1362 ggtagtaagtattccgtgctgctgttccagcacgtctctagttctcgccaatcttgatcgg 1421  
|||||

Query: 1021 atgagcgcgaaaaacctttacggtcccgagttgcgggcgtccttgagtgccccgagggga 1080  
|||||  
Sbjct: 1422 atgagcgcgaaaaacctttacggtcccgagttgcgggcgtccttgagtgccccgagggga 1481  
|||||

Query: 1081 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1140  
|||||  
Sbjct: 1482 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1541  
|||||

Query: 1141 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 1200  
|||||  
Sbjct: 1542 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 1601  
|||||

Query: 1201 agtgtactataggctgggaagtgaagacgaccccaaccgtcgccaggcgagctggcg 1260  
|||||  
Sbjct: 1602 agtgtactataggctgggaagtgaagacgaccccaaccgtcgccaggcgagctggcg 1661  
|||||

Query: 1261 ggttccaaggctcggctcgagatgctcgtcgagaggggcagcggaacgataagccccctcc 1320  
|||||  
Sbjct: 1662 ggttccaaggctcggctcgagatgctcgtcgagaggggcagcggaacgataagccccctcc 1721  
|||||

Query: 1321 ttcccagaagcggcggtgatcacctacagtccacgttggtggagctgaaacgctctgct 1380  
|||||  
Sbjct: 1722 ttcccagaagcggcggtgatcacctacagtccacgttggtggagctgaaacgctctgct 1781  
|||||

Query: 1381 ggcagcaacaaggacaaacgatctgatcgctcagacttccggcgtttctgtcgggagaga 1440  
|||||  
Sbjct: 1782 ggcagcaacaaggacaaacgatctgatcgctcagacttccggcgtttctgtcgggagaga 1841  
|||||

Query: 1441 ggcgtgcgtctggacgctgcaaaacatcgaaaaactgttttagattttcgcgcaaaagta 1500  
|||||  
Sbjct: 1842 ggcgtgcgtctggacgctgcaaaacatcgaaaaactgttttagattttcgcgcaaaagta 1901  
|||||

Query: 1501 gggaaagtttgagttttgaggtatttcaccgcaaataggttaaatgactttcgtgaaaacg 1560  
|||||  
Sbjct: 1902 gggaaagtttgagttttgaggtatttcaccgcaaataggttaaatgactttcgtgaaaacg 1961  
|||||

Query: 1561 atgtgcaatatagcggtaagactatgaaatacacaggctggacaggctgcaaaaagcaaacgg 1620  
|||||  
Sbjct: 1962 atgtgcaatatagcggtaagactatgaaatacacaggctggacaggctgcaaaaagcaaacgg 2021  
|||||

Query: 1621 gtgtggcgaccgcaaccatcactcggcgctaaaaaagcggtaaaaatttcgggtaaaaaaag 1680  
|||||  
Sbjct: 2022 gtgtggcgaccgcaaccatcactcggcgctaaaaaagcggtaaaaatttcgggtaaaaaaag 2081  
|||||

Query: 1681 atgaatctggggcatgggttatagatcctgcagaattgcacagagtgttctccatccattt 1740  
|||||  
Sbjct: 2082 atgaatctggggcatgggttatagatcctgcagaattgcacagagtgttctccatccattt 2141

Query: 1741 caaagaaatacacaccgaaacacacctaacacgcaagtatatgtgaagcgtgatgaaacacatg 1800  
|||||  
Sbjct: 2142 caaagaaatacacaccgaaacacacctaacacgcaagtatatgtgaagcgtgatgaaacacatg 2201

Query: 1801 aaatgacctcagaaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat 1860  
|||||  
Sbjct: 2202 aaatgacctcagaaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat 2261

Query: 1861 ctgatgccaggaggatcgcgacaaaatggcgcgacatggccgagcgtctttcaatttcat 1920  
|||||  
Sbjct: 2262 ctgatgccaggaggatcgcgacaaaatggcgcgacatggccgagcgtctttcaatttcat 2321

Query: 1921 caccgatgagagaggaagaccgccccctcaaaaaacaaagatggtggaagatatctgat 1980  
|||||  
Sbjct: 2322 caccgatgagagaggaagaccgccccctcaaaaaacaaagatggtggaagatatctgat 2381

Query: 1981 cctgggcttcaggagccttgccctttactggcggaacacgcgatatattgaggcacaggccc 2040  
|||||  
Sbjct: 2382 cctgggcttcaggagccttgccctttactggcggaacacgcgatatattgaggcacaggccc 2441

Query: 2041 gcactttagaggcggaagcctataaacgagtaccacacacactagaagccagattgaggaaa 2100  
|||||  
Sbjct: 2442 gcactttagaggcggaagcctataaacgagtaccacacacacactagaagccagattgaggaaa 2501

Query: 2101 atagggaaactg 2112  
|||||  
Sbjct: 2502 atagggaaactg 2513

CPU time: 0.02 user secs. 0.02 sys. secs 0.04 total secs.

Lambda K H

# Blast Result

1.33 0.621 1.12

Gapped

Lambda

K H

1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1

Number of Hits to DB: 704

Number of extensions: 18

Number of successful extensions: 13

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 2112

Length of database: 12,527,565,053

Length adjustment: 27

Effective length of query: 2085

Effective length of database: 12,527,565,026

Effective search space: 26119973079210

Effective search space used: 26119973079210

Neighboring words threshold: 0

Window for multiple hits: 0

X1: 11 (21.1 bits)

X2: 26 (50.0 bits)

X3: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 22 (43.0 bits)